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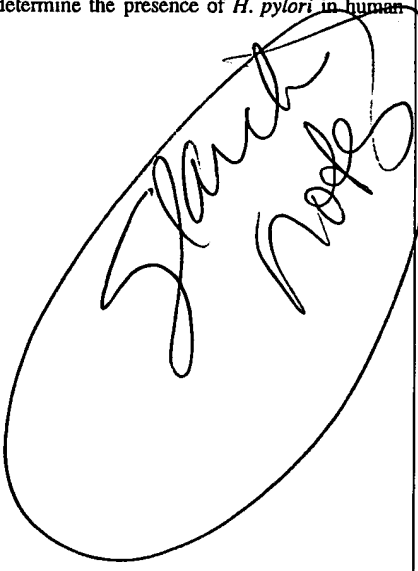
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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/54, 9/10, 15/62, C07K 16/40, G01N 33/573, C12Q 1/68, C12P 19/00 // (C12N 9/10, C12R 1:01)	A2	(11) International Publication Number: WO 98/55630 (43) International Publication Date: 10 December 1998 (10.12.98)
(21) International Application Number: PCT/CA98/00564 (22) International Filing Date: 5 June 1998 (05.06.98) (30) Priority Data: 60/048,857 6 June 1997 (06.06.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/048,857 (CIP) Filed on 6 June 1997 (06.06.97) (71) Applicant (for all designated States except US): THE GOVERNORS OF THE UNIVERSITY OF ALBERTA [CA/CA]; 222 Campus Tower, 8625-112 Street, Edmonton, Alberta T6G 2E1 (CA). (72) Inventors; and (75) Inventors/Applicants (for US only): TAYLOR, Diane, E. [CA/CA]; 3911-118 Street, Edmonton, Alberta T6J 2X2 (CA). GE, Zhongming [CA/CA]; 5112-112 Street, Edmonton, Alberta T6H 3J2 (CA).		(74) Agent: MBM & CO.; P.O. Box 809, Station B, Ottawa, Ontario K1P 5P9 (CA). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: α 1,3-FUCOSYLTRANSFERASE OF HELICOBACTER PYLORI (57) Abstract <p>A bacterial α1,3-fucosyltransferase gene and deduced amino acid sequence is provided. The gene is useful for preparing α1,3-fucosyltransferase polypeptide, and active fragment thereof, which can be used in the production of oligosaccharides such as Lewis X, Lewis Y, and sialyl Lewis X, which are structurally similar to certain tumor-associated carbohydrate antigens found in mammals. These product glycoconjugates also have research and diagnostic utility in the development of assays to detect mammalian tumors. In addition the polypeptide of the invention can be used to develop diagnostic and research assays to determine the presence of <i>H. pylori</i> in human specimens.</p> <div style="text-align: right; margin-top: 100px;"></div>		

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CLAIMS

What is claimed is:

1. A substantially purified transmembrane segment-free α 1,3-fucosyltransferase polypeptide.
- 5 2. The substantially purified transmembrane segment-free α 1,3-fucosyltransferase of claim 1, wherein the polypeptide catalyzes the synthesis of Gal β 1-4[Fuc α 1-3]GlcNAc (Lewis X) or NeuAc α 2-3-Gal β 1-4[Fuc α 1-3]GlcNAc (sialyl Lewis X).
3. The polypeptide of claim 1, wherein the polypeptide lacks α 1,4-fucosyltransferase activity.
- 10 4. The polypeptide of claim 1, wherein the polypeptide lacks α 1,2-fucosyltransferase activity.
5. The polypeptide of claim 1, wherein the polypeptide lacks α 1,4-fucosyltransferase and α 1,2-fucosyltransferase activity.
6. The polypeptide of claim 1, wherein the polypeptide has an amino acid sequence
15 selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 3.
7. An isolated polynucleotide encoding the polypeptide of claim 1.
8. The polynucleotide of claim 7, wherein the sequence encodes the amino acid sequence selected from the group SEQ ID NO:1, SEQ ID NO: 2 and SEQ ID NO: 3.

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9. A substantially purified transmembrane segment-free α 1,3-fucosyltransferase comprising a polypeptide having at least one repeat of the sequence comprising $X_1X_2LRX_3X_4Y$, wherein X_1 is D or N; X_2 is D or N; X_3 is I, V or A; X_4 is N or D.
10. A polynucleotide selected from the group consisting of:
- 5 a) SEQ ID NO: 4;
- b) SEQ ID NO: 4, wherein T is U;
- c) nucleic acid sequences complementary to a) or b); and
- d) fragments of a), b), or c) that are at least 15 nucleotide bases in length and that hybridize to DNA which encodes any one of the polypeptide set forth in SEQ
- 10 ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 3.
11. A vector containing the polynucleotide of claim 7.
12. A host cell containing the vector of claim 11.
13. An antibody which selectively binds to the polypeptide of claim 1.
14. The antibody of claim 13, wherein the antibody is monoclonal.
- 15 15. The antibody of claim 13, wherein the antibody is polyclonal.
16. A method for detecting transmembrane segment-free α 1,3-fucosyltransferase polypeptide in a sample, comprising:
- a) contacting the sample with the antibody of claim 13; and
- b) detecting binding of the antibody to α 1,3-fucosyltransferase polypeptide,
- 20 wherein binding is indicative of the presence of α 1,3-fucosyltransferase polypeptide in the sample.
17. The method of claim 16, wherein the sample is tissue.

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18. The method of claim 16, wherein the sample is a biological fluid.
19. The method of claim 16, wherein the presence of transmembrane segment-free α 1,3-fucosyltransferase polypeptide in the sample is indicative of infection by *Helicobacter pylori*.
- 5 20. The method of claim 16, wherein the presence of transmembrane segment-free α 1,3-fucosyltransferase polypeptide in the sample is indicative of the presence of malignant cells.
21. A method for detecting transmembrane segment-free α 1,3-fucosyltransferase polynucleotide in a sample, comprising:
- 10 a) contacting a sample suspected of containing α 1,3-fucosyltransferase polynucleotide with a nucleic acid probe that hybridizes to α 1,3-fucosyltransferase polynucleotide; and
- b) detecting hybridization of the probe with α 1,3-fucosyltransferase polynucleotide, wherein the detection of hybridization is indicative of
- 15 α 1,3-fucosyltransferase polynucleotide in the sample.
22. The method of claim 20, wherein the nucleic acid probe is selected from the group consisting of:
- a) a nucleic acid sequence set forth in SEQ ID NO: 4;
- b) a nucleic acid sequence set forth in SEQ ID NO: 4, wherein T is U;
- 20 c) a nucleic acid sequence complementary to a) or b); and
- d) fragments of a), b), or c) that are at least 15 nucleotide bases in length and that hybridize under stringent conditions to DNA which encodes any one of the polypeptides set forth in SEQ ID NO:1, SEQ ID NO: 2 and SEQ ID NO: 3.

32	151.5	6.3	359	1	FUT9_CANFA	Q65911	canis famil
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35	151.5	6.3	439	2	Q8AWB5	Q8awb5	gallus gall
36	151.5	6.3	479	2	Q6NTZ6	Q6ntz6	xenopus lae
37	151.5	6.3	1464	2	Q8IIF6	Q8iif6	plasmodium
38	151	6.3	168	2	Q7P9H9	Q7p9h9	rickettsia
39	150	6.3	359	2	Q8UWC1	Q8uwc1	gallus gall
40	149.5	6.3	513	1	FU12_ARATH	Q9fx97	arabidopsis
41	149	6.2	868	2	Q8IEC4	Q8iec4	plasmodium
42	148.5	6.2	2472	2	Q8IIP3	Q8iip3	plasmodium
43	148	6.2	363	2	Q6EV12	Q6ev12	xenopus tro
44	148	6.2	377	2	Q70G69	Q70g69	ipomoea nil
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ALIGNMENTS

RESULT 1

O30511

ID O30511 PRELIMINARY; PRT; 478 AA.

AC O30511;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Alpha1,3-fucosyltransferase.

GN Name=fucT;

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Helicobacter.

OX NCBI_TaxID=210;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCTC 11639;

RX MEDLINE=97407925; PubMed=9261149; DOI=10.1074/jbc.272.34.21357;

RA Ge Z, Chan N.W.C., Palcic M.M., Taylor D.E.;

RT "Cloning and heterologous expression of an alpha1,3-fucosyltransferase

RT gene from the gastric pathogen Helicobacter pylori.";

RI J. Biol. Chem. 272:21357-21363 (1997).

DR EMBL; AF008596; AAB81031.1; -

DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IRA.

KW Glycosyltransferase; Transferase.

SQ SEQUENCE 478 AA; 56070 MW; ACD47A9C7D2D3266 CRC64;

Query Match 87.1%; Score 2079; DB 2; Length 478;

Best Local Similarity 84.7%; Pred. No. 3.1e-131;

Matches 394; Conservative 15; Mismatches 26; Indels 30; Gaps 2;

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